



Search  for

as

☐ 1: CAB07811 sucrose transport protein [Vicia faba]

LOCUS CAB07811 523 aa PLN 09-APR-1997  
 DEFINITION sucrose transport protein [Vicia faba].  
 ACCESSION CAB07811  
 PID g1935019  
 VERSION CAB07811.1 GI:1935019  
 DBSOURCE embl locus VFZ93774, accession Z93774.1  
 KEYWORDS .  
 SOURCE fava bean.  
 ORGANISM Vicia faba  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicia.  
 REFERENCE 1 (residues 1 to 523)  
 AUTHORS Weber,H., Borisjuk,L., Heim,U., Sauer,N. and Wobus,U.  
 TITLE A role for sugar transporters during seed development: Molecular  
 characterization of a hexose and a sucrose carrier in faba bean  
 seeds  
 JOURNAL Plant Cell In press  
 REFERENCE 2 (residues 1 to 523)  
 AUTHORS Heim,U.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-APR-1997) Heim U., Institut fuer Pflanzengenetik und  
 Kulturpflanzenforschung, Correnstr.3, Gatersleben, FRG  
 FEATURES Location/Qualifiers  
 source 1..523  
 /organism="Vicia faba"  
 /db\_xref="taxon:3906"  
 /dev\_stage="middle"  
 /tissue\_type="cotyledon"  
 Protein 1..523  
 /function="sugar transport"  
 /product="sucrose transport protein"  
 CDS 1..523  
 /gene="sut"  
 /db\_xref="SPTREMBL:004077"  
 /coded\_by="Z93774.1:5..1576"  
 ORIGIN  
 1 meplsstkqi nnnnlnakps slhvetqple psplrkimvv asiaagvqfg walqlslltp  
 61 yvqllgihht waayiwlcgp isgmlvqpiv gyhsdrctsr fgrrrpfiaa gsiavaiafv  
 121 ligyaadlgh sfgdsldqkv rpraigifvv gfwildvann mlggpcrall gdlcagnqrk  
 181 trnanaffsf fmavgnvlgy aagaysklyh vfpftktkac nvycanlksc fflsialltv  
 241 latsaliyvk etaltpektv vttdggssg gmpcfqqlsg afkelkrpmw illlvtclnw  
 301 iawfpfllfd tdwmgkevyg gtvgeghayd mgvregalg mlsvvlgat slgvdilarg  
 361 vggvkrllgi vnflaiclgt ltlvtklaq hsrqyapgtg algdplppse gikagaltlf  
 421 svlgvplait ysipfalasi fsstsgaggg lslgvlnlai vipqmfvsvl sgpwdalfgg  
 481 gnlpafvuga vaalasgils iillpspppd maksvsatgg gfh  
 //



Search  Protein  for

Display  Default View  as HTML  Save  Add to Clipboard

☐ 1: CAA76367 **sucrose/H<sup>+</sup> symporter [Daucus carota]**

LOCUS CAA76367 501 aa PLN 13-JAN-1999  
 DEFINITION sucrose/H<sup>+</sup> symporter [Daucus carota].  
 ACCESSION CAA76367  
 PID g2969887  
 VERSION CAA76367.1 GI:2969887  
 DBSOURCE embl locus DCSUT1A, accession Y16766.1  
 KEYWORDS .  
 SOURCE carrot.  
 ORGANISM Daucus carota  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

REFERENCE 1 (residues 1 to 501)  
 AUTHORS Shakya,R. and Sturm,A.  
 TITLE Characterization of source- and sink-specific sucrose/H<sup>+</sup> symporters from carrot  
 JOURNAL Plant Physiol. 118 (4), 1473-1480 (1998)  
 MEDLINE 99063785

REFERENCE 2 (residues 1 to 501)  
 AUTHORS Sturm,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-MAR-1998) A. Sturm, Friedrich Miescher-Institut, Maulbeerstr. 66, CH-4058 Basel, SWITZERLAND

FEATURES Location/Qualifiers  
 source 1..501  
 /organism="Daucus carota"  
 /cultivar="Namtaise"  
 /db\_xref="taxon:4039"  
 /dev\_stage="12 week old plants"  
 /tissue\_type="leaves"  
 Protein 1..501  
 /product="sucrose/H<sup>+</sup> symporter"  
 CDS 1..501  
 /gene="SUT1a"  
 /db\_xref="SPTREMBL:O65929"  
 /coded\_by="Y16766.1:114..1619"

ORIGIN  
 1 magpeadrnr hrggataapp prsrvsrlrl lrvasvacgi qfgwalqlsl ltpyvqelgi  
 61 phawssiiwl cgplsgllvq pivghmsdq tskygrrrpf ivaggtaiil aviiiahsad  
 121 iggllgdtad nktmaivafv igfwildvan nmtggpcral ladltgndar rtrvanayfs  
 181 lfmaignvlg yatgaysgwy kvfpfsltss ctincanlks afyidiifii ittyisisaa  
 241 kerprissqd gpqfsedgta qsghieafl welfgtfrll pgsvwvillv tclnwigwfp  
 301 filfdtdwmg reiyggepnq ggsysdgvrm gafglmmnsv vlgitsvlme klcriwgsf  
 361 mwglslnilmt icffamllit fiaknmdygt npppngivis alivfailgi plaitysvpy  
 421 alvstriesl glggglsmgv lnlaivvpqv ivslgsgpwd qlfgggnspa fvvaalsafa  
 481 aglialiair rprvdksrhl h

//



Search	Protein	▼	for		Go	Clear
Display	Default View	▼	as	HTML	▼	Save
				Add to Clipboard		

☐ 1: S43142      **sucrose transport protein - castor bean**

LOCUS            S43142            533 aa            PLN            26-MAY-2000  
DEFINITION    sucrose transport protein - castor bean.  
ACCESSION     S43142  
PID            g542020  
VERSION       S43142    GI:542020  
DBSOURCE      pir: locus S43142;  
              summary: #length 533 #molecular-weight 56359 #checksum 5859;  
              superfamily: common tobacco sucrose transport protein;  
              PIR dates: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change  
              26-May-2000.  
KEYWORDS      .  
SOURCE        castor bean.  
ORGANISM      Ricinus communis  
              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
              Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
              Malpighiales; Euphorbiaceae; Ricinus.  
REFERENCE     1 (residues 1 to 533)  
AUTHORS       Weig, A. and Komor, E.  
TITLE          Direct Submission  
JOURNAL       Submitted (??-MAR-1994) to the EMBL Data Library  
FEATURES  
    source                    Location/Qualifiers  
                              1..533  
                              /organism="Ricinus communis"  
                              /db\_xref="taxon:3988"  
    Protein                   1..533  
                              /product="sucrose transport protein"  
                              /note="sucrose carrier"  
ORIGIN  
    1 mqsstskenk qppssqphpp plmvagaaep nssplrkvvm vasiaagiqf gwalqlslit  
    61 pyvqllgiph twaafiwlcg pismvlvqpi vgyhsdrcts rfgrrrpfia sgaafvaiav  
    121 fligyaadlg hlsgdslaks pktraiaifv vgfwildvan nmlqgpcral ladlsgtsqk  
    181 ktrtanalfs ffmavgnvlg yaagaythly klfpftkttt cdvycanlks cffisivlll  
    241 sltvlalsyv kekpwsdpqa vdnaeddtas qasssaqmp ffgelgafk nlkrpmwill  
    301 lvtclnwiaw fpfllfdtdw mgrevyggds sgaeqlkly drgvragalg lmlnsvlvgf  
    361 tslgvevlar gvggvkrlwg ivnfvlavcl amtvlvtkqa estrrfatvs ggakvplppp  
    421 sgvkagalal favmgvpqai tysipfalas ifsntsgagq glslgvlnlv ivipqmivsv  
    481 aagpwwdalfg ggnlpafvvg avaalasgif altmlpsppq dmpsakalta afh

//



Protein

Search Protein  for   Display Default View  as HTML  Save Add to Clipboard☐ 1: BAA24071 sucrose transporter [Oryza sativa]

LOCUS BAA24071 537 aa PLN 26-DEC-1997  
 DEFINITION sucrose transporter [Oryza sativa].  
 ACCESSION BAA24071  
 PID g2723471  
 VERSION BAA24071.1 GI:2723471  
 DBSOURCE locus D87819 accession D87819.1  
 KEYWORDS .  
 SOURCE Oryza sativa.  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE 1 (residues 1 to 537)  
 AUTHORS Hirose, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-SEP-1996) to the DDBJ/EMBL/GenBank databases. Tatsuro  
 Hirose, Hokuriku National Agricultural Experiment Station, Lab. of  
 Rice Metabolism; 1-2-1 Inada, Joetsu, Niigata 943-01, Japan  
 (E-mail: dragon@affrc.go.jp, Tel: 0255-26-8300, Fax: 0255-24-8578)  
 REFERENCE 2 (sites)  
 AUTHORS Hirose, T., Imaizumi, N., Scofield, G. N., Furbank, R. T. and Ohsugi, R.  
 TITLE cDNA cloning and tissue specific expression of a gene for sucrose  
 transporter from rice (Oryza sativa L.)  
 JOURNAL Plant Cell Physiol. 38 (12), 1389-1396 (1997)  
 MEDLINE 98182940  
 FEATURES Location/Qualifiers  
 source 1..537  
 /organism="Oryza sativa"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:4530"  
 /clone="pSTP1-1"  
 /tissue\_type="green leaf"  
 Protein 1..537  
 /product="sucrose transporter"  
 CDS 1..537  
 /gene="OsSUT1"  
 /coded\_by="D87819.1:67..1680"

## ORIGIN

```

1 margsgaggg gggggggglel svvgvggggar gggggeaaaa vetaapislg rliisgmvag
61 gvqygwalql sltptyvqtl glshaltsfm wlcgpiagmv vqpcvglysd rctskwgrrr
121 pyiltgcvli clavvvgfs adigyamgdt kedcsvyhgs rwhaaivvyl gfwlldfsnn
181 tvqgparalm adlsgrhpgg tansifcswm amgnilgyss gstnnwhkwf pflktracce
241 acanlkgafl vavifslcl vitlifakev pfgknaalpt ksnepaepg tgplavlkgf
301 rnlptgmpsv livtgltwls wfpfilydtd wmgreiyhgd pkgtdpqiea fnqgvragaf
361 glllnsivlg fssfliepmc rkvgprvvwv tsnflvciam aatalisfws lkdfhgtvqk
421 aitadksika vclvlfafg vplavlysvp favtaqlaat rggggqlctg vlnisivipq
481 vvialgagpw delfgkgnip afglasgfal iggvagifll pkiskrqfws vsmgggh

```

//